

E. Lazar-Wesley

11
9/23/02

RAW SEQUENCE LISTING

DATE: 09/23/2002

PATENT APPLICATION: US/09/639,273

TIME: 12:47:34

Input Set : N:\Crf3\RULE60\09639273.raw

Output Set: N:\CRF4\09232002\I639273.raw

-----SEQUENCE LISTING-----

3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: Innes, Michael
6 Creasey, Abba
8 (ii) TITLE OF INVENTION: Production of Tissue Factor Pathway
9 Inhibitor
11 (iii) NUMBER OF SEQUENCES: 7
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Chiron Corporation
15 (B) STREET: 4560 Horton St.
16 (C) CITY: Emeryville
17 (D) STATE: CA
18 (E) COUNTRY: USA
19 (F) ZIP: 94608
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30B
27 (vi) CURRENT APPLICATION DATA:
C--> 28 (A) APPLICATION NUMBER: US/09/639,273
C--> 29 (B) FILING DATE: 15-Aug-2000
30 (C) CLASSIFICATION:
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: US/08/286,530
35 (B) FILING DATE: 05-AUG-1994
37 (viii) ATTORNEY/AGENT INFORMATION:
38 (A) NAME: Savereide, Paul B.
39 (B) REGISTRATION NUMBER: 36,914
40 (C) REFERENCE/DOCKET NUMBER: 0991.001
42 (ix) TELECOMMUNICATION INFORMATION:
43 (A) TELEPHONE: 510-601-2585
44 (B) TELEFAX: 510-655-3542
47 (2) INFORMATION FOR SEQ ID NO: 1:
49 (i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 1065 base pairs
51 (B) TYPE: nucleic acid
52 (C) STRANDEDNESS: double
53 (D) TOPOLOGY: linear
55 (ii) MOLECULE TYPE: other nucleic acid
57 (iii) HYPOTHETICAL: NO
59 (iv) ANTI-SENSE: NO
62 (ix) FEATURE:

ENTERED

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63          (A) NAME/KEY: CDS
64          (B) LOCATION: 1..1056
67          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
69 ATG CAG ATC TTC GTC AAG ACT TTG ACC GGT AAA ACC ATA ACA TTG GAA      48
70 Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
71   1           5           10           15
73 GTT GAA TCT TCC GAT ACC ATC GAC AAC GTT AAG TCG AAA ATT CAA GAC      96
74 Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ser Lys Ile Gln Asp
75           20           25           30
77 AAG GAA GGT ATC CCT CCA GAT CAA CAA AGA TTG ATC TTT GCC GGT AAG      144
78 Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
79           35           40           45
81 CAG CTA GAA GAC GGT AGA ACG CTG TCT GAT TAC AAC ATT CAG AAG GAG      192
82 Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
83   50           55           60
85 TCC ACC TTA CAT CTT GTG CTA AGG CTC CGC GGT GGT GAT TCT GAG GAA      240
86 Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Asp Ser Glu Glu
87  65           70           75           80
89 GAT GAA GAA CAC ACA ATT ATC ACA GAT ACG GAG TTG CCA CCA CTG AAA      288
90 Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
91           85           90           95
93 CTT ATG CAT TCA TTT TGT GCA TTC AAG GCG GAT GAT GGC CCA TGT AAA      336
94 Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys
95           100           105           110
97 GCA ATC ATG AAA AGA TTT TTC TTC AAT ATT TTC ACT CGA CAG TGC GAA      384
98 Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
99           115           120           125
101 GAA TTT ATA TAT GGG GGA TGT GAA GGA AAT CAG AAT CGA TTT GAA AGT      432
102 Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
103           130           135           140
105 CTG GAA GAG TGC AAA AAA ATG TGT ACA AGA GAT AAT GCA AAC AGG ATT      480
106 Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg Ile
107 145           150           155           160
109 ATA AAG ACA ACA TTG CAA CAA GAA AAG CCA GAT TTC TGC TTT TTG GAA      528
110 Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu Glu
111           165           170           175
113 GAA GAT CCT GGA ATA TGT CGA GGT TAT ATT ACC AGG TAT TTT TAT AAC      576
114 Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn
115           180           185           190
117 AAT CAG ACA AAA CAG TGT GAA CGT TTC AAG TAT GGT GGA TGC CTG GGC      624
118 Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly
119           195           200           205
121 AAT ATG AAC AAT TTT GAG ACA CTG GAA GAA TGC AAG AAC ATT TGT GAA      672
122 Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu
123           210           215           220
125 GAT GGT CCG AAT GGT TTC CAG GTG GAT AAT TAT GGA ACC CAG CTC AAT      720
126 Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn
127 225           230           235           240
129 GCT GTG AAT AAC TCC CTG ACT CCG CAA TCA ACC AAG GTT CCC AGC CTT      768

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130 Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val Pro Ser Leu
131          245          250          255
133 TTT GAA TTT CAC GGT CCC TCA TGG TGT CTC ACT CCA GCA GAC AGA GGA      816
134 Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly
135          260          265          270
137 TTG TGT CGT GCC AAT GAG AAC AGA TTC TAC TAC AAT TCA GTC ATT GGG      864
138 Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly
139 ----- 275 ----- 280 ----- 285 -----
141 AAA TGC CGC CCA TTT AAG TAC AGT GGA TGT GGG GGA AAT GAA AAC AAT      912
142 Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn
143          290          295          300
145 TTT ACT TCC AAA CAA GAA TGT CTG AGG GCA TGT AAA AAA GGT TTC ATC      960
146 Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile
147 305          310          315          320
149 CAA AGA ATA TCA AAA GGA GGC CTA ATT AAA ACC AAA AGA AAA AGA AAG      1008
150 Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys
151          325          330          335
153 AAG CAG AGA GTG AAA ATA GCA TAT GAA GAA ATT TTT GTT AAA AAT ATG      1056
154 Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val Lys Asn Met
155          340          345          350
157 TGAGTCGAC      1065
160 (2) INFORMATION FOR SEQ ID NO: 2:
162 (i) SEQUENCE CHARACTERISTICS:
163 (A) LENGTH: 352 amino acids
164 (B) TYPE: amino acid
165 (D) TOPOLOGY: linear
167 (ii) MOLECULE TYPE: protein
169 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
171 Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
172 1          5          10          15
174 Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ser Lys Ile Gln Asp
175          20          25          30
177 Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
178          35          40          45
180 Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
181          50          55          60
183 Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Asp Ser Glu Glu
184 65          70          75          80
186 Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
187          85          90          95
189 Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys
190          100          105          110
192 Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
193          115          120          125
195 Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
196          130          135          140
198 Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg Ile
199 145          150          155          160
201 Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu Glu

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202          165          170          175
204 Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn
205          180          185          190
207 Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly
208          195          200          205
210 Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu
211          210          215          220
213 Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn
214 225          230          235          240
216 Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val Pro Ser Leu
217          245          250          255
219 Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly
220          260          265          270
222 Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly
223          275          280          285
225 Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn
226          290          295          300
228 Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile
229 305          310          315          320
231 Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys
232          325          330          335
234 Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val Lys Asn Met
235          340          345          350
238 (2) INFORMATION FOR SEQ ID NO: 3:
240 (i) SEQUENCE CHARACTERISTICS:
241 (A) LENGTH: 276 amino acids
242 (B) TYPE: amino acid
243 (C) STRANDEDNESS: single
244 (D) TOPOLOGY: linear
246 (ii) MOLECULE TYPE: peptide
251 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
253 Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu
254 1 5 10 15
256 Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp
257 20 25 30
259 Gly Pro Cys Arg Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr
260 35 40 45
262 Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn
263 50 55 60
265 Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn
266 65 70 75 80
268 Ala Asn Arg Ile Ile Lys Thr Thr Leu Gln Glu Lys Pro Asp Phe
269 85 90 95
271 Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg
272 100 105 110
274 Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly
275 115 120 125
277 Gly Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys
278 130 135 140

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280   Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly
281   145                               150                               155                               160
283   Thr Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys
284                               165                               170                               175
286   Val Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro
287                               180                               185                               190
289   Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn
290                               195                               200                               205
292   Ser Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly
293   210                               215                               220
295   Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys
296   225                               230                               235                               240
298   Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys
299                               245                               250                               255
301   Arg Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe
302                               260                               265                               270
304   Val Lys Asn Met
305   275

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307 (2) INFORMATION FOR SEQ ID NO: 4:

309 (i) SEQUENCE CHARACTERISTICS:

310 (A) LENGTH: 9 base pairs

311 (B) TYPE: nucleic acid

312 (C) STRANDEDNESS: single

313 (D) TOPOLOGY: linear

315 (ii) MOLECULE TYPE: other nucleic acid

316 (A) DESCRIPTION: /desc = "primer"

321 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

323 CCGCGGGGC

9

325 (2) INFORMATION FOR SEQ ID NO: 5:

327 (i) SEQUENCE CHARACTERISTICS:

328 (A) LENGTH: 23 base pairs

329 (B) TYPE: nucleic acid

330 (C) STRANDEDNESS: single

331 (D) TOPOLOGY: linear

333 (ii) MOLECULE TYPE: other nucleic acid

334 (A) DESCRIPTION: /desc = "primer"

339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

341 GCTCCGCGGT GGCGATTCTG AGG

23

343 (2) INFORMATION FOR SEQ ID NO: 6:

345 (i) SEQUENCE CHARACTERISTICS:

346 (A) LENGTH: 24 base pairs

347 (B) TYPE: nucleic acid

348 (C) STRANDEDNESS: single

349 (D) TOPOLOGY: linear

351 (ii) MOLECULE TYPE: other nucleic acid

352 (A) DESCRIPTION: /desc = "primer"

357 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

359 TCTGTCGACT CACATATTTT TAAC

24

361 (2) INFORMATION FOR SEQ ID NO: 7:

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/639,273

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Input Set : N:\Crf3\RULE60\09639273.raw
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 160
Seq#:2; Line(s) 238
Seq#:3; Line(s) 307
Seq#:4; Line(s) 325
Seq#:5; Line(s) 343
Seq#:6; Line(s) 361

VERIFICATION SUMMARY

DATE: 09/23/2002

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Input Set : N:\Crf3\RULE60\09639273.raw

Output Set: N:\CRF4\09232002\I639273.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]